Computers and Biomedical Research **32,** 322–335 (1999)
Article ID cbmr.1999.1518, available online at http://www.idealibrary.com on IDEAL®

# The Identification of Peaks in Physiological Signals

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Received February 17, 1998

The identification of peaks is fundamental in the processing of physiological signals. For example, it is common to the analysis of electrocardiograms, electroencephalograms, sympathetic neuronal activity, pulse oximetry, respiratory movement, hormone pulse secretion, and even chromatography. Often it is necessary to detect peaks in real time, but the task is frequently complicated by baseline wander and other interference. Current approaches to the problem tend to be complicated, specific to a particular domain, and reliant on several tunable parameters. There is a need for a simple and general mathematical formalization of peaks and troughs that has easily examinable properties and is readily implementable as an efficient algorithm. In this paper we present such a mathematical model together with an algorithm for the detection of peaks and troughs. We illustrate the generality of the method with some actual physiological data. 

*Key Words:* peak detection; formal specification; algorithm; electrocardiogram.

## INTRODUCTION

Medical research and modern clinical practice increasingly involve the recording of continuous physiological signals (*1*). A fundamental task in the analysis of such signals is the detection of peaks and troughs: for example, the components of the electrocardiogram (*2*), the waves of the electroencephalogram (*3*), sympathetic neuronal activity in experimental animals (*4, 5*), respiratory peak inspiration and end-expiration (*6*), pulses of episodic hormone secretion (*7*), and the spectral peaks of the chromatograph (*8*). Often it is necessary to detect peaks in real time, but the task is frequently complicated by baseline wander and other types of interference.

In some applications, if the signal is adequately smoothed, it is sufficient simply to identify all local maxima: an example is the counting of smooth muscle contractions (*9*). However, in many applications the signal to noise ratio in the frequency band of interest is low. In these circumstances a statistical approach is often used to determine whether a significant rise or fall in the signal level has occurred, for example when monitoring sympathetic neuronal activity (*4, 5*) or analyzing sequential hormone assays (*7, 10*). The null hypothesis is that there is no change



0010-4809/99 $30.00

in the signal level. A peak is thus characterized by a significant rise followed by a significant fall in the signal level. Alternatively, in the absence of a statistical model, an empirical threshold is set: for example, in one approach to electroencephalogram analysis a peak has been defined as a sample that is greater than both its predecessor and its successor by a predetermined threshold amount (*3*). This local definition of a peak overcomes the problem of baseline drift. A variation of the method entails maintaining three adjacent sliding windows: a peak is detected if the average of the middle window is greater (by some threshold) than the averages of the two adjacent ones (*11, 12*). Rather than define peaks and troughs locally, many peak detection algorithms first remove the baseline variation (if present) and then define a peak as a threshold excursion above the baseline. Examples are the detection of QRS complexes in electrocardiograms (*13*), the detection of pulses of hormone secretion (*14*), the identification of ultrasound echoes (*15*), and the analysis of peaks in the frequency spectrum of lung sounds (*16*). A straightforward way of removing baseline variation is to convolve the signal with a differentiating (and possibly smoothing) filter: peaks and troughs can then be identified as zero crossings. For example, this has been successful in electrocardiogram analysis (*17, 18*) and in the identification of end-inspiration in respiratory movement recordings (*6*), although differentiation does tend to amplify high frequency noise. More sophisticated approaches to peak detection include pattern recognition by means of neural networks. For example, this has been employed for the analysis of peaks in infrared spectra (*19*).

In summary, therefore, although there are many different approaches to peak detection they tend to be rather complicated and they are often tailored to a particular domain, for example, electrocardiogram analysis (*20*). On the other hand, more generally applicable methods typically depend on numerous tunable parameters, for example (*21*) and (*22*), both of which require no less than four user-selected values. A simple and general mathematical definition of peaks and troughs is needed that has easily examinable properties and is readily implementable as an efficient algorithm. This requirement is perhaps underlined by one comparative empirical study (*7*) of eight pulse-detection programs for hormone assay analysis: three of the eight programs were found to produce roughly similar results to each other but were distinct from the other five. Moreover, even the three most concordant programs failed to identify the same particular peaks on approximately 28% of occasions.

In this paper we present a simple mathematical formalization of a “peak” and a “trough” that should be relevant to a wide range of physiological applications. The model is declarative in character and is defined in just a few lines. The properties of the model are examined by means of lemmas and seen to be intuitive. A total of 14 lemmas are stated without proof: all follow easily from the respective definitions and are simple manipulations in logic and set theory. (Details can be found in (*23*).) For convenience we adopt the notational conventions of the *Z* specification language because they are fully documented elsewhere (*24*); we provide a brief glossary of *Z* symbols in the appendix. We also present an efficient and easily programmed algorithm for identifying the peaks and troughs in a signal in accordance with the model and we illustrate the generality of the method with some actual physiological data. A strength of the algorithm is that it entails only a single pass along the input signal and so is suitable for on-line use for real-time identification of peaks and troughs.

## FORMALISM

First consider a "physiological signal." It comprises a finite number of sequential discrete samples of some variable of interest. For example, a single channel electrocardiogram is a sequence of samples of the voltage on one particular lead, usually at a fixed frequency of 250 or 500 Hz; a sequential hormone assay is a series of measurements of the circulating level of a particular hormone, usually at fixed intervals of say 10 min; a respiratory movement recording is a sequence of samples of the voltage across a transducer, usually at a fixed frequency of about 20 Hz.

Since all measurements are in practice made with finite precision, any physiological sample can, with suitable scaling, be represented by an integer. For simplicity therefore, we regard a physiological *signal* as a sequence of integers:

$$\text{Signal} \triangleq \mathsf{seq}\ \mathbb{Z}. \qquad [1]$$

Consider now the nature of a peak in a signal. Let $q$ be an arbitrary signal and let indices $i$ and $j$ refer to arbitrary elements (samples) in $q$. A peak in $q$ is a maximal element that locally "dominates" its surroundings by some positive, predetermined threshold ($\delta$). We say that element $j$ *dominates* element $i$ precisely when $q[j]$ exceeds $q[i]$ by at least $\delta$ and the signal between $i$ and $j$ is bounded below by $q[i]$ and above by $q[j]$. This last requirement captures the notion of the domination being "local." Let $i \overset{\delta}{\underset{q}{<}} j$ mean that in signal $q$ element $i$ is dominated by a subsequent element $j$. Correspondingly, let $j \overset{\delta}{\underset{q}{>}} i$ mean that element $i$ is dominated by a preceding element $j$:

$$\_\_ < \_\_,\ \_\_ > \_\_ : \mathbb{N}_1 \rightarrow \text{Signal} \rightarrow \mathbb{N} \leftrightarrow \mathbb{N} \qquad [2]$$

$\forall \delta : \mathbb{N}_1;\ q : \text{Signal};\ i, j : \mathbb{N} \bullet$

$$i \overset{\delta}{\underset{q}{<}} j \quad \Leftrightarrow \quad 1 \leq i \leq j \leq \#q \quad \wedge \quad q[i] + \delta \leq q[j] \quad \wedge \quad q(|i \mathrel{..} j|) \subseteq (q[i] \mathrel{..} q[j])$$

$$j \overset{\delta}{\underset{q}{>}} i \quad \Leftrightarrow \quad 1 \leq j \leq i \leq \#q \quad \wedge \quad q[i] + \delta \leq q[j] \quad \wedge \quad q(|j \mathrel{..} i|) \subseteq (q[i] \mathrel{..} q[j]).$$

A *peak* element of $q$ is any element that dominates both a preceding element and a subsequent element. Correspondingly, a *trough* element is any element that is dominated both by a preceding element and by a subsequent element. Let $\pi_\delta(q)$ and $\tau_\delta(q)$ denote, respectively, the peak and the trough elements of $q$:

$$
\begin{gathered}
\pi,\ \tau : \mathbb{N}_1 \to \text{Signal} \to \mathbb{P}\mathbb{N} \\
\forall\, \delta : \mathbb{N}_1;\ q : \text{Signal} \bullet \\
\pi_\delta(q) = \mathsf{ran}\ (\overset{\delta}{\underset{q}{<}}) \cap \mathsf{dom}\ (\overset{\delta}{\underset{q}{>}}) \\
\tau_\delta(q) = \mathsf{ran}\ (\overset{\delta}{\underset{q}{>}}) \cap \mathsf{dom}\ (\overset{\delta}{\underset{q}{<}}).
\end{gathered} \qquad [3]
$$

## SOME LEMMAS

Notice first that domination is a strict partial order (irreflexive, antisymmetric, and transitive).

*Lemma 1. Irreflexivity*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad (\overset{\delta}{\underset{q}{>}}) \cap \mathsf{id} = \{\ \} \quad \wedge \quad (\overset{\delta}{\underset{q}{<}}) \cap \mathsf{id} = \{\ \}.$$

*Lemma 2. Antisymmetry*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad (\overset{\delta}{\underset{q}{>}}) \cap (\overset{\delta}{\underset{q}{>}})^{-1} = \{\ \} \quad \wedge \quad (\overset{\delta}{\underset{q}{<}}) \cap (\overset{\delta}{\underset{q}{<}})^{-1} = \{\ \}.$$

*Lemma 3. Transitivity*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad (\overset{\delta}{\underset{q}{>}}) \fatsemi (\overset{\delta}{\underset{q}{>}}) \subseteq (\overset{\delta}{\underset{q}{>}}) \quad \wedge \quad (\overset{\delta}{\underset{q}{<}}) \fatsemi (\overset{\delta}{\underset{q}{<}}) \subseteq (\overset{\delta}{\underset{q}{<}}).$$

Notice that no element can simultaneously dominate to the left and be dominated from the left. Similarly, no element can simultaneously dominate to the right and be dominated from the right.

*Lemma 4. Exclusivity*:

$$
\begin{aligned}
\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad & \mathsf{ran}\ (\overset{\delta}{\underset{q}{>}}) \cap \mathsf{ran}\ (\overset{\delta}{\underset{q}{<}}) \\
& = \{\ \} \quad \wedge \quad \mathsf{dom}\ (\overset{\delta}{\underset{q}{>}}) \cap \mathsf{dom}\ (\overset{\delta}{\underset{q}{<}}) = \{\ \}.
\end{aligned}
$$

It therefore follows that no element can be both a peak and a trough.

*Lemma 5. Uniqueness*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad \pi_\delta(q) \cap \tau_\delta(q) = \{\ \}$$

Consider a mirror function $\mu$ that reflects the indices of a sequence:

$$\mu \triangleq \lambda q : \text{Signal} \bullet \lambda i : \mathsf{dom}\ q \bullet \#q - i + 1. \qquad [4]$$

Thus $\mu(q) ⨾ q$ is the reverse of sequence $q$ and $\mu(q) ⨾ \mu(q)$ is the identity function on the domain of $q$.

It follows that the peaks (respectively troughs) of a reversed signal are the mirror image of the peaks (respectively troughs) of the original signal. In other words, peak and trough identification commute with reflection.

*Lemma 6. Reflection*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad \mu(q)(\!|\, \pi_\delta(q) \,|\!) = \pi_\delta(\mu(q) ⨾ q) \quad \wedge \quad \mu(q)(\!|\, \tau_\delta(q) \,|\!) = \tau_\delta(\mu(q) ⨾ q).$$

Similarly, consider an inversion function $\eta$ that negates integers:

$$\eta \triangleq \lambda z : \mathbb{Z} \bullet -z. \qquad [5]$$

Thus $q ⨾ \eta$ is the inversion of sequence $q$.

It follows that the peaks (respectively troughs) of an inverted signal are the troughs (respectively peaks) of the original signal.

*Lemma 7. Inversion*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \quad \eta(\!|\, \pi_\delta(q) \,|\!) = \tau_\delta(q ⨾ \eta) \quad \wedge \quad \eta(\!|\, \tau_\delta(q) \,|\!) = \pi_\delta(q ⨾ \eta).$$

The left and right domination relations enlarge monotonically as the threshold is lowered.

*Lemma 8. Antimonotonicity of domination*:

$$\delta, \varepsilon : \mathbb{N}_1;\ q : \text{Signal} \mid \delta \leq \varepsilon \vdash \quad (\overset{\delta}{\underset{q}{>}}) \supseteq (\overset{\delta}{\underset{q}{>}}) \quad \wedge \quad (\overset{\delta}{\underset{q}{<}}) \supseteq (\overset{\delta}{\underset{q}{<}}).$$

Consequently the set of peak (respectively trough) elements enlarges monotonically as the threshold is lowered.

*Lemma 9. Antimonotonicity of peaks and troughs*:

$$\delta, \varepsilon : \mathbb{N}_1;\ q : \text{Signal} \mid \delta \leq \varepsilon \vdash \quad \pi_\delta(q) \supseteq \pi_\varepsilon(q) \quad \wedge \quad \tau_\delta(q) \supseteq \tau_\varepsilon(q).$$

Furthermore, the left and right domination relations enlarge monotonically as the signal is extended.

*Lemma 10. Monotonicity of domination*:

$$\delta : \mathbb{N}_1;\ p, q : \text{Signal} \mid p \leq q \vdash \quad (\overset{\delta}{\underset{p}{>}}) \subseteq (\overset{\delta}{\underset{q}{>}}) \quad \wedge \quad (\overset{\delta}{\underset{p}{<}}) \subseteq (\overset{\delta}{\underset{q}{<}}).$$

Therefore the peaks (respectively troughs) of a signal are a superset of the peaks (respectively troughs) of any prefix of the signal.

*Lemma 11. Monotonicity of peaks and troughs*:

$$\delta : \mathbb{N}_1;\ p, q : \text{Signal} \mid p \leq q \vdash \quad \pi_\delta(p) \subseteq \pi_\delta(q) \quad \wedge \quad \tau_\delta(p) \subseteq \tau_\delta(q).$$

If a signal is extended then any newly created peak lies after any peak or trough in the original signal.

*Lemma 12. Peak creation*:

$$\begin{aligned}\delta : \mathbb{N}_1;\ p, q : \text{Signal};\ i, j : \mathbb{N} \mid p \leq q \quad &\wedge \quad i \in (\pi_\delta(p) \cup \tau_\delta(p)) \\ &\wedge \quad j \in (\pi_\delta(q) - \pi_\delta(p)) \vdash i < j.\end{aligned}$$

Similarly, if a signal is extended then any new trough also lies after any peak or trough in the original signal.

*Lemma 13. Trough creation*:

$$\begin{aligned}\delta : \mathbb{N}_1;\ p, q : \text{Signal};\ i, j : \mathbb{N} \mid p \leq q \quad &\wedge \quad i \in (\pi_\delta(p) \cup \tau_\delta(p)) \\ &\wedge \quad j \in (\tau_\delta(q) - \tau_\delta(p)) \vdash i < j.\end{aligned}$$

However, neither the first nor the last element of a signal can be a peak or trough.

*Lemma 14. Containment*:

$$\delta : \mathbb{N}_1;\ q : \text{Signal} \vdash \pi_\delta(q) \subseteq (2 \mathinner{.\,.} (\#q - 1)) \quad \wedge \quad \tau_\delta(q) \subseteq (2 \mathinner{.\,.} (\#q - 1)).$$

## AN ALGORITHM

Table 1 shows a procedure ($PT$) that computes the peak ($P$) and trough ($T$) elements of the signal ($Q$) that is given as the first argument. Local variable $i$ is used as an index into $Q$, counting from the first element ($Q[1]$) to the last element ($Q[\#Q]$). Within the while loop, variable $d$ indicates the direction of the signal:

$d = \uparrow$ . . . proceeding from a trough to a peak,

$d = \downarrow$ . . . proceeding from a peak to a trough,

$d = ?$ . . . direction indeterminate.

Variable $a$ records the index of a maximal element since the last trough. Correspondingly, variable $b$ records the index of a minimal element since the last peak. Variable $S$ records the indices (there may be more than one) of the maximal elements since the last trough if the signal is rising ($d = \uparrow$) or those of the minimal elements since the last peak if the signal is falling ($d = \downarrow$). The threshold $\delta$ is assumed to be a global constant.

In order to understand how the algorithm works, consider first the case that during execution of the body of the loop the current direction of the signal is up ($d = \uparrow$). Notice that if the current element $Q[i]$ is strictly greater than the previous

TABLE 1

Procedure PT for Computing Peaks and Troughs

```
procedure PT (value Q : Signal; result P, T: ℙℕ) ≜
    var S: ℙℕ a, b, i : ℕ d: {?, ↑, ↓} ●
    P, T, S, a, b, i, d := { }, { }, { }, 1, 1, 0, ?;
    do i ≠ # Q →
        i := i + 1;
        if d = ?   → if   Q[a] ≥ Q[i] + δ → d := ↓
                     [ ]  Q[i] ≥ Q[b] + δ → d := ↑
                     fi;
                     if   Q[a] < Q[i] → a := i
                     [ ]  Q[i] < Q[b] → b := i
                     fi;
                     S := {i}
        [ ] d = ↑ → if   Q[a] < Q[i]      → S, a := {i}, i
                     [ ]  Q[a] = Q[i]      → S := S ∪ {i}
                     [ ]  Q[a] ≥ Q[i] + δ → P, S, b, d := P ∪ S, {i}, i, ↓
                     fi
        [ ] d = ↓ → if   Q[i] ≤ Q[b]      → S, b := {i}, i
                     [ ]  Q[i] = Q[b]      → S := S ∪ {i}
                     [ ]  Q[i] ≥ Q[b] + δ → T, S, a, d := T ∪ S, {i}, i, ↑
                     fi
        fi
    od
```

highest level $Q[a]$ since the last trough then both $S$ and $a$ are updated. If the current element is equal to the previous highest level then it too is maximal and its index is added to the others in set $S$. If the current element is strictly less than the previous highest then no action is taken unless the current element is $\delta$ or more below the previous highest. In the later case the current element is dominated by all the members of $S$ which are all equivalent peak elements since they also dominate at least one previous trough element. A peak having now been passed, the direction $d$ is reversed and the current element is the unique minimal element since the last peak. (The case that $d = \uparrow$ is similar.) The algorithm thus continues to alternate between peak and trough detection as the direction switches back and forth. This oscillatory process begins immediately when an element is encountered that is at least $\delta$ above or below some previous element.

Notice that there is no requirement that individual peak elements alternate with individual trough elements: for example, if a peak has a flat top then all its maximal elements are peak elements. Often we do not wish to enumerate the indices of all the maximal elements of a peak or all the minimal elements of a trough, but would rather place a single representative marker on each peak and trough. Algorithm *PT* is easily modified to identify just the last maximal element of each peak and last minimal element of each trough: replace the assignment $P, S, b, d := P \cup S, \{i\}, i, \downarrow$ by $P, b, d := P \cup \{i\}, i, \downarrow$ and make a similar change to the corresponding assignment $T, S, a, d := T \cup S, \{i\}, i, \uparrow$. Set $S$ is then redundant and should therefore be eliminated from the algorithm thus saving the overhead of implementing a set type. If all occurrences of $<$ are replaced by $\leq$ then the algorithm computes the first rather than the last of each set of peak and trough elements. However, the choice of first or last seems arbitrary and the symmetry embodied in Lemma 6 is of course lost. Better alternatives are to compute either the mid-point between the first and last elements or the mean of the indices, although neither of these is necessarily an integer. The mean is computed by simply replacing $S$ with two integer-type variables, one of which stores the sum of the elements in $S$ and the other of which stores the cardinality of $S$. The median point is a third alternative, but computation of the median does of course require that all the points in set $S$ are stored temporarily during each peak/trough phase.

## SOME EXAMPLES

### *Respiratory Excursions*

Application of the algorithm is best illustrated with some examples of actual physiological data. Figure 1 shows part of a recording of the respiratory movements of a neonate who exhibits intermittent apnea. Transducers were placed on both the

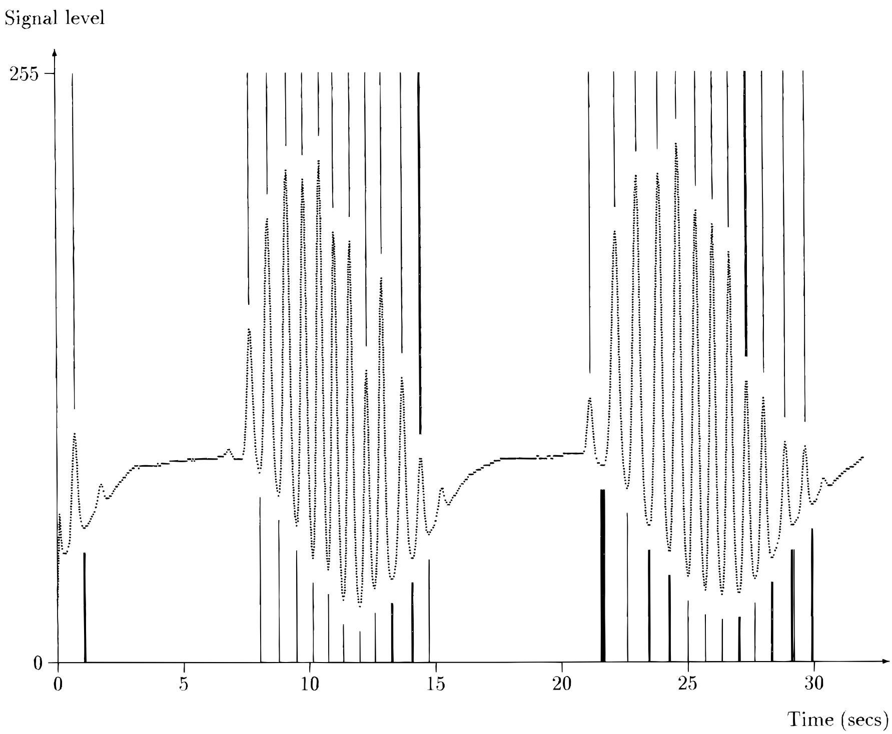


**FIG. 1.** Neonatal chest movement recording (8-bit data sampled at 20 Hz) showing peaks and troughs as detected with threshold $\delta = 20$.

chest and the abdomen: the displayed signal represents the sum of the outputs of the two sensors. The measurements are on an integral scale 0 to 255 with a sampling frequency of 20 Hz. The peak and trough elements were identified using procedure *PT* with a threshold ($\delta$) of 20; they are marked, respectively, by vertical lines above and below the tracing. Each thick vertical line represents a cluster of adjacent peak elements or adjacent trough elements. Notice that some of the smaller peaks and troughs (those whose height is less than 20) are missed: the parameter $\delta$ should be set to the height of the smallest peak or trough that should be detected.

Figure 2 shows the same recording as Fig. 1 but marked with a threshold of 2 rather than 20. Notice that all significant peaks and troughs are now identified. Notice also that the peak and trough elements are a superset of those identified with $\delta = 20$ (Lemma 9).

*Electrocardiogram QRS Complex Detection*

The peak detection algorithm has more general application. One approach to the identification of particular features in a signal is to transform the signal by application of a feature identification function. The task of identifying the features

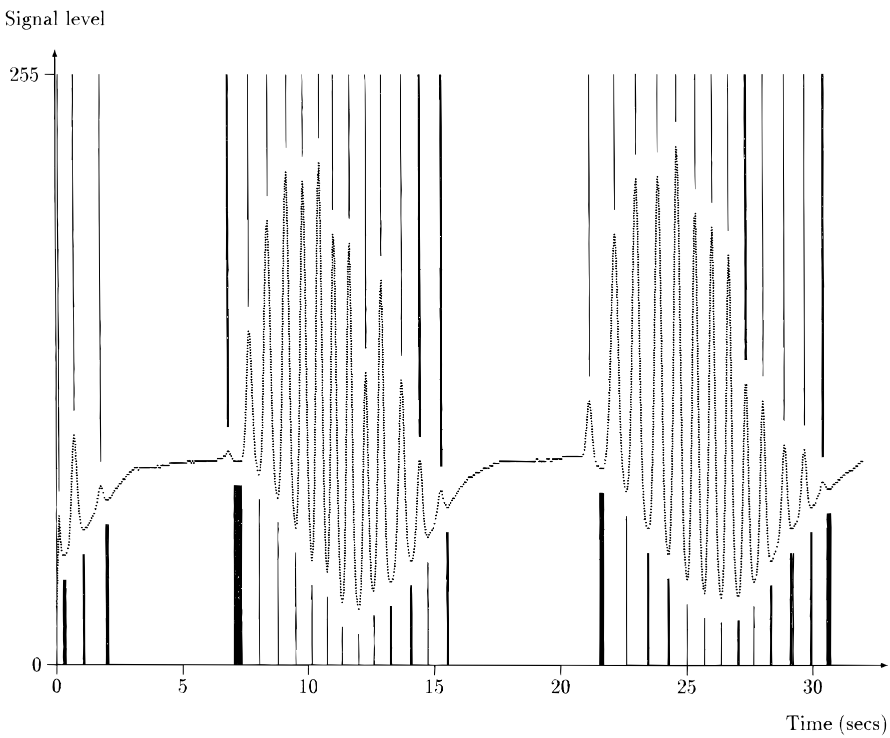


**FIG. 2.** Neonatal chest movement recording (corresponding to Fig. 1) showing peaks and troughs as detected with threshold $\delta = 2$.

then becomes one of identifying peaks in the transformed signal. For example, the usual transformation used in the identification of QRS complexes in electrocardiograms is to rectify and smooth the first or second derivatives (*25*, *26*), or the sum of the two (*27*). Simple threshold methods are usually employed for detecting peaks in the transformed signal since baseline wander is largely eliminated by derivative transformation. However, the peak detection algorithm described in this paper is possibly more robust because the peaks of the transformed signal may have irregular shapes that otherwise cause confusion. We illustrate this with an example.

Figure 3 shows a portion of a child's electrocardiogram sampled at 100 Hz. The $T$ waves are rather pronounced and there is incidentally a gross movement artifact. Figure 4 shows the same signal after a derivative transformation has been applied. The transformation entails squaring and then smoothing the second derivative. The second derivative of signal $q$ at position $i$ is given simply by $q[i-1] - 2q[i] + q[i+1]$. Smoothing is achieved by convolving with an equilateral triangular kernel of width 0.1 s (about the duration of a QRS complex) at its mid-point (i.e., 0.2 s at its base). Variations in the sizes of the peaks is then reduced by taking the square root of all elements of the transformed signal. Notice how stable the transformed signal is despite the movement artifact in the original signal: each large peak

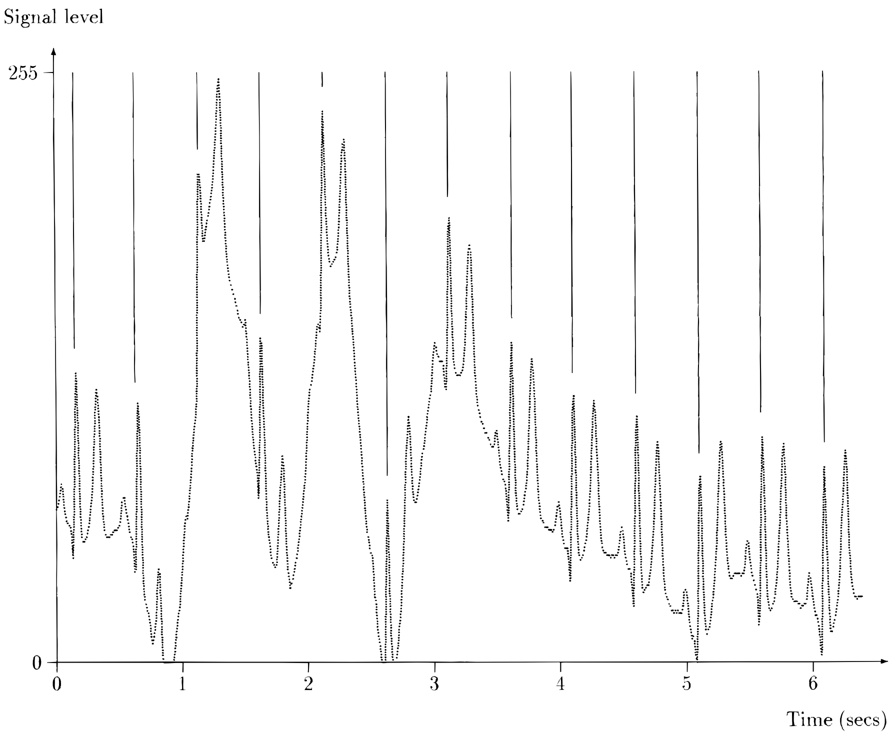


**FIG. 3.** Electrocardiogram of a child with tachycardia (8-bit data sampled at 100 Hz) showing a large movement artifact.

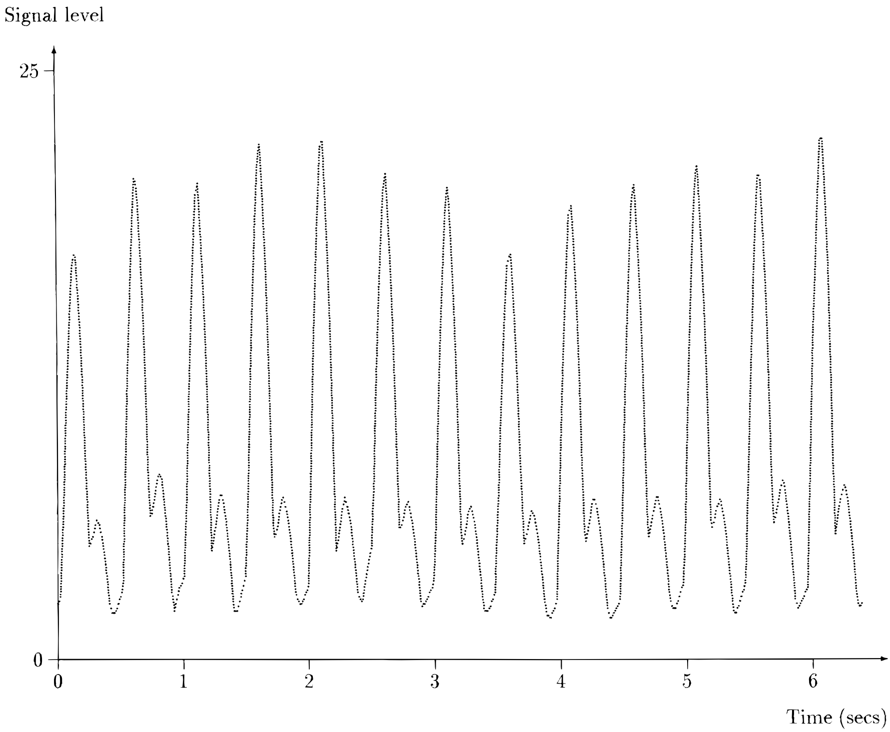


**FIG. 4.** Transformation of the ECG shown in Fig. 3 by smoothing the squared second derivative and then taking the square root: each large peak corresponds to a *QRS* complex and each small peak corresponds to a *T* wave.

corresponds to a QRS complex. Notice also that on the falling edge of each large peak is a small peak that corresponds to the T wave. Although the absolute level of the small peaks is about 30% or so of that of the large peaks, the rising edges of the small peaks are less than 10% of the length of the rising edges of the large peaks. Since the objective is to detect the large peaks (QRS complexes) while rejecting the small peaks (T waves), our algorithm is likely to discriminate between the two kinds of peak better than a fixed threshold above the baseline: the vertical lines marking the QRS complexes in Fig. 3 are those obtained by applying the peak detection algorithm to the transformed signal shown in Fig. 4 with a threshold ($\delta$) of 5.

## DISCUSSION

In this paper we have presented a formal mathematical definition of peaks and troughs in a signal. We have then enumerated and examined the properties of the model by means of lemmas. The model is logically equivalent to an earlier definition proposed by Marshall (*28*), but has a different structure that suggests a different implementation. Marshall's model was developed with the analysis of chromatograph spectra in mind. In that application it is often necessary to generate "threshold plots" of the number of peaks against the threshold employed for peak detection. Marshall's algorithm entails multiple passes through the data, successively eliminating the smallest peaks. This is quite feasible of course for the analysis of chromatograph peaks. However, our algorithm requires only one pass and so is suitable for continuous on-line physiological monitoring too. Indeed, as we have shown, our peak detection algorithm has a potentially wide application, not only to the identification of the maxima and minima in physiological signals, but also to on-line feature identification via signal transformation.

The usual kind of transformations employed entail rectification and smoothing of first or second derivatives of the original signal. Such transformations are used for the identification of the start of inspiration in respiratory recordings (*6*) and in particular for the detection of QRS complexes in electrocardiograms (*26*, *29*). Usually the transformations are invariant to signal inversion and commute with signal reflection. Since our peak detection algorithm also commutes with signal reflection (Lemma 6), our entire QRS detector shares the two properties too. This corresponds to the familiar, empirical observation that a QRS complex remains just as recognizable to the human eye when the electrocardiogram is turned upside down or even viewed in a mirror. Not all QRS detection algorithms, however, have this intuitive property (e.g., (*13*)), especially if latency periods are included in the peak detection algorithm: (*26*) lists several examples. However, derivative transformations are by no means the only kind used for physiological feature identification. For example, neural networks form the basis of a rather different method of QRS detection (*30*, *31*). A perceptron is used as a predictive filter that models the *P* and *T* waves but does not model the QRS: the QRS is thus signalled by a large error signal.

We now intend to try the peak detection algorithm in as wide a range of applications as possible. The simplicity of the algorithm makes it ideal for implementation in hardware. Coupled with suitable transformations, this holds promise for continuous on-line monitoring of heart rate and other physiological variables in the ambulatory and intensive care setting.

## APPENDIX: GLOSSARY

The following glossary should enable anyone unfamiliar with the *Z* specification language to read the formal sections of this paper.

| | |
|---|---|
| $\mathbb{N}_1$ | The set of all nonzero natural numbers ($= \mathbb{N} - \{0\}$). |
| $m \mathrel{..} n$ | *The set of natural numbers from m* up to *n* inclusive. |
| $S \leftrightarrow T$ | *The set of all relations between S* and *T*. |
| $S \rightarrow T$ | *The set of all total functions from S* to *T*. |
| $S \nrightarrow T$ | *The set of all partial functions from S* to *T*. |
| $\{x : T \mid P \bullet t\}$ | The set of all terms *t* over variable(s) *x* drawn from *T* such that predicate *P* holds (if present). Term *t* may be omitted if identical to *x*. |

| | |
|---|---|
| $\lambda x : T \mid P \bullet t$ | The function mapping to terms $t$ the variable(s) $x$ drawn from $T$ such that predicate $P$ holds (if present). This is identical to the set $\{x : T \mid P \bullet (x, t)\}$. |
| id | The identity function ($= \lambda x : T \bullet x$) on given type $T$. |
| seq $S$ | The set of all finite sequences of elements drawn from $S$. (In "$Z$" a sequence is regarded as a function from an initial segment of the nonzero natural numbers to the set of all possible elements.) |
| $q[n]$ | The $n$th element ($= q(n)$) of sequence $q$. |
| $\#q$ | The cardinality (i.e., length) of sequence $q$. |
| dom $r$ | The set of all elements in the domain of relation (or function) $r$. |
| ran $r$ | The set of all elements in the range of relation (or function) $r$. |
| $r \fatsemi s$ | The forward composition of relations (or functions) $r$ and $s$. |
| $r(\lvert S \rvert)$ | The image of set $S$ through relation (or function) $r$. |
| $r^{-1}$ | The inverse $\{x : S; y : T \mid (x, y) \in r \bullet (y, x)\}$ of relation (or function) $r$. |

## ACKNOWLEDGMENTS

We thank Paul Johnson for his invaluable help and constructive comments in the preparation of this paper.

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